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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/645,706	08/24/2000	Keith V. Wood	341.005US1	3329

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EXAMINER	
PROUTY, REBECCA E	
ART UNIT	**PAPER NUMBER**
1652	

DATE MAILED: 09/13/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/645,706	WOOD ET AL.	
	Examiner	Art Unit	
	Rebecca E. Prouty	1652	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on _____.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *See Continuation Sheet* is/are pending in the application.

4a) Of the above claim(s) 64 is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1,3-6,9,11,12,15,18,20,21,24-39,41-45,47,60,67,69-71,74,76-78,80-88 and 90-96* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date 7/06.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

Continuation of Disposition of Claims: Claims pending in the application are 1,3-6,9,11,12,15,18,20,21,24-39,41-45,47,60,64,67,69-71,74,76-78,80-88 and 90-96.

Claims 2, 7, 8, 10, 13, 14, 16, 17, 19, 22, 23, 40, 46, 48-59, 61-63, 65, 66, 68, 72, 73, 75, 79, and 89 have been canceled. Claims 1, 3-6, 9, 11, 12, 15, 18, 20, 21, 24-39, 41-45, 47, 60, 64, 67, 69-71, 74, 76-78, 80-88, 90-94 and newly presented claims 95-96 are still at issue and are present for examination.

Claim 64 remains withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected species, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the response filed 11/18/02.

Applicants' arguments filed on 6/22/06, have been fully considered. Rejections and/or objections not reiterated from previous office actions are hereby withdrawn.

Claims 90, 95, and 96 are objected to because of the following informalities: the word "to" needs to be inserted following "selected" in the phrase "codons are selected reduce the number of identified sequences or sites". Appropriate correction is required.

Claims 1, 3-6, 9, 11, 12, 15, 18, 20, 21, 24-39, 41-45, 47, 60, 67, 69-71, 74, 76-78, 80-83, 85-88, and 90-96 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for

failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 1 (from which claims 3-6, 9, 11, 12, 15, 20, 21, 24-39, 41-45, 60, 69, 70 81, 86, and 90 depend), 47 (from which claims 71, 82, and 87 depend), 67 (from which claims 69, 70, 81, 88 and 95 depend), 74 (from which claims 76, 77, 81, 88 and 96 depend), and 78 (from which claims 80, 82, and 87 depend) are vague and indefinite in the recitation of "a reduced number of a combination of mammalian transcription factor binding sequences, intron splice sites, poly(A) addition sites and/or prokaryotic 5' noncoding regulatory sequences", "wherein the mammalian transcription factor binding sequences are present in a database of transcription factor binding sequences" and "known mammalian transcription factor binding sequences". The rejection was described in the previous Office Action.

Applicants argue that the terms "transcription factor binding sequences", "intron splice sites", "poly(A) addition sites" and "prokaryotic 5' noncoding regulatory sequences" are conventional in the art and argue that these terms are in fact used in the reference cited by the examiner in the 103 rejection. This is acknowledged. However, in the art these terms define a group of sequences related by function. The art does not define clearly **what** sequences are included in the

group. Since applicants invention requires a skilled artisan to **quantify** the number of such sequences it is imperative that the artisan know explicitly what sequences are to be included and what sequences are not so one can in fact count them. While the art clearly defines **some** specific sequences which fall into each group (for example AAUAAA as a polyadenylation sequence) many other sequences may have the same function and not all such sequences are known and taught by the art.

With regard to calculating the number of mammalian transcription factor binding sequences, intron splice sites, poly(A) addition sites and prokaryotic 5' noncoding regulatory sequences, point to Example 1 of the specification and the declaration of Dr. Wood submitted with the instant response and argue that both evidence that contrary to the Examiner's assertion, the calculation of the number of transcription factor binding sequences, intron splice sites, poly(A) addition sites and prokaryotic 5' noncoding regulatory sequences in a particular sequence is possible. However, it has never been the examiner's contention that given a clear set of sequences to be searched that calculation of the number was not possible, but that the claims are indefinite absent a clear definition of what sequences are encompassed by these terms. In Example 1 of the specification it is clearly set forth that transcription factor

binding sequences were mammalian sequences identified in the SITE table of TRANSFAC database version 3.2 having a minimum length of 5 nucleotides and a minimum log-likelihood (as defined in the spec.) of 10, intron splice sites were AGGTRAGT, AGGTRAG or YNCAGG, poly(A) addition sites were AATAAA, and prokaryotic 5' noncoding regulatory sequences were TATAAT or either of AGGA or GGAG paired with an ATG codon within 12 or fewer bases 3' to said sequence. Each of these is a clearly identifiable and defined set of sequences, presuming that the SITE table of the TRANSFAC database version 3.2 is obtainable. Similarly in the search discussed in the declaration of Dr. Wood, transcription factor binding sites are defined as mammalian sequences identified in the SITE table of TRANSFAC database version 4.0 having a minimum length of 5 nucleotides and a minimum log-likelihood (as defined in the TESS software literature attached) of 10. This is a clearly identifiable and defined set of sequences, presuming that the SITE table of TRANSFAC database version 4.0 is obtainable. However, none of applicants claims is limited in a similar fashion. It is suggested that applicants limit the claims to the sites used in Example 1 of the specification and submit a copy of the SITE table of version 3.2 of the TRANSFAC database.

Claim 18 as amended is confusing in the recitation "or the complement thereof which encodes a luciferase" as the complement does not encode a luciferase.

Claims 47 and 83 as amended are indefinite in the recitation of "corresponding wild type nucleic acid sequence" as it is unclear to what sequences this must refer. Is this limited to the wild type sequences from which SEQ ID NOS: 9, 18, 297, and 301 were derived (i.e., Luc*Ppl*YG, SEQ ID NO:1) or to any wild type beetle luciferase gene?

Claim 83 is confusing in the recitation of "hybridizes under medium stringency hybridization conditions to SEQ ID NO:22 (Rluc-final) … and comprises an open reading frame encoding a luciferase with 90% amino acid sequence identity to a beetle luciferase" as SEQ ID NO:22 (Rluc-final) is a variant of *Renilla* luciferase which is not a beetle luciferase and in view of the lack of similarity of *Renilla* luciferase with beetle luciferases, a polynucleotide which hybridizes to SEQ ID NO:22 could not encode a luciferase with 90% amino acid sequence identity to a beetle luciferase. While applicants amended claim 47 to address this problem they did not amend claim 83. As such this rejection is maintained for claim 83.

Claims 1, 3-6, 9, 11, 12, 15, 20-21, 24-33, 35-39, 41-45, 47, 60, 67, 69, 70, 81-82, 86-88, and 90-95 are rejected under

35 U.S.C. 112, first paragraph, because the specification, while being enabling for (1) a variant of a parent DNA molecule encoding a reporter polypeptide identical to a reporter polypeptide encoded by said parent DNA, having more than 25% of the codons altered and having a reduced number of transcription factor binding sequences, intron splice sites, poly(A) addition sites and promoter sequences than a mammalian codon optimized variant of the parent nucleic acid, (2) a variant of a parent DNA molecule encoding a luciferase having 90% identity to the polypeptide encoded by SEQ ID NO:2 and having more than 25% of the codons altered and having a reduced number of transcription factor binding sequences, intron splice sites, poly(A) addition sites and 5' noncoding regulatory sequences than a mammalian codon optimized variant of SEQ ID NO:2 or (3) to any nucleic acid which will hybridize to SEQ ID NO:9 under high stringency conditions and encode a polypeptide having luciferase activity, does not reasonably provide enablement for any variant DNA molecules encoding any reporter polypeptide having at least 90% identity to a wild type reporter polypeptide, having more than 25% of the codons altered and having a reduced number of transcription factor binding sequences, intron splice sites, poly(A) addition sites and 5' noncoding regulatory sequences than a mammalian codon optimized version of the parent nucleic

acid or to any nucleic acid which will hybridize to SEQ ID NO:9 under medium stringency conditions. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to use the invention commensurate in scope with these claims. The rejection is explained in the previous Office Action.

Applicants first state that it is unclear how Applicant's specification teaches one of skill in the art how to make and use a variant of a parent DNA molecule encoding a reporter polypeptide identical to a reporter polypeptide encoded by said parent DNA, having more than 25% of the codons altered and having a reduced number of transcription factor binding sequences, intron splice sites, poly(A) addition sites and promoter sequences if the art worker would not recognize or understand sequences that are mammalian transcription factor binding sequences, intron splice sites, poly(A) addition sites and prokaryotic 51 noncoding regulatory sequences. Applicants are in fact correct that, if a skilled artisan cannot clearly identify these sites, he can not practice the invention as taught. However, for the instant rejection the claims were examined as best possible ignoring this problem (as it is clearly addressed by the rejection above) in the interest of compact prosecution, such that all possible problems could be

identified concurrently. The instant rejection would be maintained even if the claims clearly identified all such sites for the reasons presented.

Next applicants argue that with respect to reporter polypeptides, such as GFP, beetle luciferase, GUS, CAT, and beta-lactamase, applicant has provided evidence that it is well within the skill of the art to introduce substitutions into various reporter proteins and yield a variant protein with the activity of the corresponding wild-type reporter protein. However, it is noted that the evidence applicants refer to is available for specific GFPs, beetle luciferases, GUS or CAT enzymes, and beta-lactamases but each of these groups of reporter polypeptides includes vast numbers of proteins which are not well characterized and often substantially different from those taught in the art. For example there are many different luminescent beetle species but only a few firefly and click beetle luciferases are well characterized in the art and even these enzymes differ from each other enormously. The rejected claims are not limited the nucleic acids encoding reporters exhibiting high similarity to only those reporters which are well characterized (Note claims that are so limited such as claims 18, 71, 74, 76-78, 80, 83-85, and 96 are not rejected).

Finally applicants argue that one of skill in the art in possession of applicant's specification is readily able to determine whether a variant nucleic acid molecule hybridizes under medium stringency conditions to Applicant's synthetic polynucleotides and has an open reading frame encoding a beetle luciferase polypeptide which has at least 90% amino acid sequence identity to a luciferase encoded by a corresponding wild type nucleic acid sequence, and having a reduced number of transcription factor binding sequences, intron splice sites, poly(A) addition sites and 5' noncoding regulatory sequences than a mammalian codon optimized version of the parent nucleic acid. However, while methods of determining if any individual sequence would have the properties described are well known in the art, methods of determining which sequences from the virtually infinite genus of sequences capable of hybridizing to under medium stringency conditions to the recited nucleic acids and encoding a protein having 90% identity to any beetle luciferase actually are within the scope of the instant claims (i.e., encode a luciferase protein) beyond just making and testing all possibilities are not provided. While enablement is not precluded by the necessity for routine screening, if a large amount of screening is required, the specification must provide a reasonable amount of guidance with respect to the direction in

which the experimentation should proceed. Such guidance has **not** been provided in the instant specification.

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claims 1, 3-6, 9, 11, 12, 15, 20, 21, 24-39, 41-45, 60, 67, 69, 70, 81, 86 and 90-95 are rejected under 35 U.S.C. 103(a) as being unpatentable over Sherf et al. (US Patent 5,670,356) in view of Zolotukhin et al. (US Patent 5,874,304), Donnelly et al. (WO 97/47358), Pan et al., Cornelissen et al. (US Patent 5,952,547), and Hey et al. (US Patent 6,169,232). The rejection is explained in the previous Office Action.

Applicants argue that the combination of references does not disclose or suggest Applicant's invention as each reference discloses a different wav to modify the coding sequence of a

different gene to increase expression. This is not persuasive because each of these references is drawn to methods of increasing the expression of a gene in a desired host by altering the sequence of the nucleic acid but not the encoded protein in a variety of ways which will lead to increases in the production of desired protein. The cited references show that the art was clearly aware that a combination of changes in codon preference and removal of sequences detrimental to transcription and/or translation in either the wild type gene or the codon optimized version can be used to accomplish this goal. While each of the cited references used a different combination of types of modifications, the art clearly teaches all of the claimed modifications encompassed in applicants claims (i.e., mammalian codon optimization, removal of transcription factor binding sequences, removal of splice sites, removal of potential promoters, and removal of polyadenylation sites) and clearly teaches combinations of them with one or more of the others.

Applicants argue that while there is a general teaching in the combination of cited documents to alter codons and/or remove certain undesired sequences in a selected sequence, none of the cited documents teaches or suggests that codon alterations, to prepare a sequence with codons employed more frequently in an evolutionarily divergent organism optionally in conjunction with

removal of restriction enzyme sites, ATTTA sequences, splice sites, polyA sites, A or T strings, CG dinucleotides in adjacent codons, prokaryotic promoters, inverted repeats and prokaryotic factor-independent RNA polymerase terminators, may create transcription factor binding sites and none of the cited documents discloses or suggests removal of transcription factor binding sites from a codon optimized gene. While it is true that none of the cited documents explicitly teach that codon replacements may create unwanted transcription factor binding sequences not present in the wild type sequence, Hey et al., Donnelly et al. and Pan et al. all show that the art recognized that codon modifications can **introduce** sequences which are unwanted within the synthetic gene, that additional codon modifications can decrease the introduction of those sequences and Sherf et al. clearly teach that the presence of transcription factor binding sequences within a reporter gene is an unwanted feature as it may interfere with the desired genetic neutrality of the reporter gene (see column 8). Furthermore, it is obvious on its face that anytime a gene sequence is altered that one necessarily creates new sequences which were not previously present and that merely by random chance some of these newly created sequences may be detrimental. It is even further obvious on its face that the more changes one makes, the

higher the chances that such a detrimental sequence will be introduced. Sherf et al. made only limited changes to codon selection and thus at least in his explicit teachings focused on the elimination of detrimental sequences present in the wild type sequence. However, the remaining art clearly would have motivated one of skill in the art to make more substantial changes in codon preference within the luciferase of Sherf et al. Furthermore the disclosures of Hey et al., Donnelly et al. and Pan et al. would have clearly led a skilled artisan to scan not only the wild type sequence for the unwanted transcription factor binding sites but also the codon optimized version thereof.

Applicants argue that to arrive at applicant's invention, one of skill in the art in possession of the cited documents would need to choose to identity specifically transcription factor binding sites, promoter sequences, splice sites, and polyA sites, as sequences to be removed by codon replacement although the references also teach removal of internal palindromic sequences, restriction endonuclease sites, glycosylation sites, ATTTA sequences, RNA polymerase termination signals, TA and CG doublets, blocks of G or C residues, inverted repeats, and long runs of purines. However, this is not persuasive as applicants claims are not drawn to any combination

in particular and do not exclude removal of other detrimental sequences in addition to those specifically recited in the claims and the art clearly teaches several combinations of these.

Applicants argue that none of the cited documents discloses or suggests the use of software to identify particular regulatory sites, such as mammalian transcription factor binding sequences, in a database of transcription factor binding sequences. However, this is not persuasive as most of applicants claims do not even mention the use of software to identify sites to be removed. Furthermore, even for those claims that do mention this, it is noted that the claims recite products not processes. Patentability of a product recited in product-by-process format is determined by the characteristics of the product itself not by the recited method. A nucleic acid in which the sites to be removed were identified by an undefined computer program would not differ in any respect from a nucleic acid in which the sites to be removed were identified by any other method.

Applicants finally argue that one of ordinary skill in the art in possession of the cited art would have no reasonable expectation that any particular set of changes would improve activity in a gene that is to be expressed in a highly

evolutionarily distinct cell. This is not persuasive because the art clearly provide an expectation that codon optimization and the elimination of a variety of types of sequences which are detrimental to transcription and/or translation will improve the expression of a gene in a heterologous host. While it is acknowledged that one cannot be certain that the modifications will not have unexpected consequences, applicants are reminded that obviousness does not require an absolute certainty of success but only a reasonable expectation thereof.

Claims 18, 47, 71, 74, 76-78, 80, 82-85, 87, 88 and 96 are rejected under 35 U.S.C. 103(a) as being unpatentable over Sherf et al. (US Patent 5,670,356) in view of Zolotukhin et al. (US Patent 5,874,304), Donnelly et al. (WO 97/47358), Pan et al., Cornelissen et al. (US Patent 5,952,547), and Hey et al. (US Patent 6,169,232) as applied to claims 1, 3-6, 9, 11, 12, 15, 20, 21, 24-39, 41-45, 60, 67, 69, 70, 81, 86 and 90-95 above, and further in of Wood et al. (WO 99/14336). The rejection is explained in the previous Office Action.

Applicant has not presented any arguments specifically traversing this rejection but instead relies upon the traversal discussed above. Therefore, this rejection is maintained for the reasons presented above.

The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. A nonstatutory obviousness-type double patenting rejection is appropriate where the conflicting claims are not identical, but at least one examined application claim is not patentably distinct from the reference claim(s) because the examined application claim is either anticipated by, or would have been obvious over, the reference claim(s). See, e.g., In re Berg, 140 F.3d 1428, 46 USPQ2d 1226 (Fed. Cir. 1998); In re Goodman, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); In re Longi, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); In re Van Ornum, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); In re Vogel, 422 F.2d 438, 164 USPQ 619 (CCPA 1970); and In re Thorington, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) or 1.321(d) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent either is shown to be commonly owned with this application, or claims an invention made as a result of activities undertaken within the scope of a joint research agreement.

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

Claims 91, 93 and 94 are provisionally rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claims 1-50 and 58-60 of copending Application No. 10/314,827. Although the conflicting claims are not identical, they are not patentably distinct from each other. The rejection is explained in the previous Office Action.

Applicants argue that the claims in the present application are directed to synthetic nucleic acid molecules for

chloramphenicol acetyltransferase, Renilla luciferase, beetle luciferase, beta-lactamase, beta-glucuronidase or beta-galactosidase while the claims of 10/314,827 are directed to 10/314,827) are directed to synthetic nucleic acid molecules for a fluorescent polypeptide. However, it is noted that applicants have not amended claims 91, 93 and 94 of the instant application to synthetic nucleic acid molecules for chloramphenicol acetyltransferase, Renilla luciferase, beetle luciferase, beta-lactamase, beta-glucuronidase or beta-galactosidase. These claims recite synthetic nucleic acid molecules encoding any reporter polypeptide which clearly includes the fluorescent polypeptides of the copending application.

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL.** See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

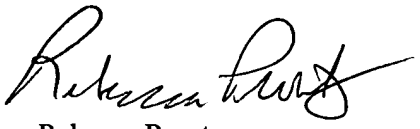
A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will

expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Rebecca E. Prouty whose telephone number is 571-272-0937. The examiner can normally be reached on Tuesday-Friday from 8 AM to 5 PM. The examiner can also be reached on alternate Mondays

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathapura Achutamurthy, can be reached at (571) 272-0928. The fax phone number for this Group is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).



Rebecca Prouty
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Art Unit 1652